VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION:

Paragraph beginning at page 4, line 22, has been amended as follows:

– Figure 1 (SEQ ID NO:1) shows an embodiment of a nucleic acid (mRNA) which includes a sequence which encodes a breast cancer protein provided herein, BCO2 (SEQ ID NO:2). The start (ATG) and stop (TGA) codons are underlined, defining the open reading frame. –

Paragraph beginning at page 4, line 25, has been amended as follows:

– Figure 2 (SEQ ID NO:2) shows an embodiment of an amino acid sequence of BCO2. –

Paragraph beginning at page 4, line 29, has been amended as follows:

– Figures 4A and 4B show the alignment of human BCO2 amino acid sequence (SEQ ID NO:2) and the amino acid sequence of the mouse BCO2 ortholog (SEQ ID NO:3). –

Paragraph beginning at page 6, line 6, has been amended as follows:

– In a preferred embodiment, the breast cancer sequences are those of nucleic acids encoding BCO2 or fragments thereof. Preferably, the breast cancer sequence is that depicted in figure 1 (SEQ ID NO:1), or a fragment thereof. Preferably, the breast cancer sequences encode a protein having the amino acid sequence depicted in figure 2 (SEQ ID NO:2), or a fragment thereof. –

Paragraph beginning at page 11, line 5, has been amended as follows:

– The extracellular domains of transmembrane proteins are diverse; however, conserved motifs are found repeatedly among various extracellular domains. Conserved structure and/or functions have been ascribed to different extracellular motifs. For example, cytokine receptors are characterized by a cluster of cysteines and a WSXWS (W= tryptophan, S= serine, X=any amino acid) motif (SEQ ID NO:4). Immunoglobulin-like

domains are highly conserved. Mucin-like domains may be involved in cell adhesion and leucine-rich repeats participate in protein-protein interactions. –

Paragraph beginning at page 12, line 26, has been amended as follows:

– In a preferred embodiment, the sequences which are used to determine sequence identity or similarity are selected from the sequences set forth in the figures, preferably that shown in ~~Figures 1~~ Figure 1 (SEQ ID NO:1) and fragments thereof. In one embodiment the sequences utilized herein are those set forth in the figures. In another embodiment, the sequences are naturally occurring allelic variants of the sequences set forth in the figures. In another embodiment, the sequences are sequence variants as further described herein. –

Paragraph beginning at page 13, line 18, has been amended as follows:

– Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical with the nucleotide residues of figure 1 (SEQ ID NO:1). A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively. –

Paragraph beginning at page 41, line 15, has been amended as follows:

– In a preferred embodiment, as outlined above, screens may be done on individual genes and gene products (proteins). That is, having identified a particular breast cancer gene as important in a particular state, screening of modulators of either the expression of the gene or the gene product itself can be done. The gene products of breast cancer genes are sometimes referred to herein as "breast cancer proteins" or "breast cancer modulating proteins" or "BCMP". Additionally, "modulator" and "modulating" proteins are sometimes used interchangeably herein. In one embodiment, the breast cancer protein is termed BCO2. BCO2 sequences can be identified as described herein for breast cancer sequences. In one embodiment, a BCO2 protein sequence is as depicted in Figure 2

(SEQ ID NO:2). The breast cancer protein may be a fragment, or alternatively, be the full length protein to the fragment shown herein. Preferably, the breast cancer protein is a fragment. In a preferred embodiment, the amino acid sequence which is used to determine sequence identity or similarity is that depicted in figure 2. In another embodiment, the sequences are naturally occurring allelic variants of a protein having the sequence depicted in figure 2. In another embodiment, the sequences are sequence variants as further described herein. –

On page 60, immediately preceding the claims, the enclosed Sequence Listing was added to the text.